### Ltd 5.1.6 Compugen GenCore version (c) 1993 - 2004 Copyright

updates/sec Seconds .864 8 ; Search time 153.86 (without alignments) 1187.234 Million cell 02:56:08 sw model 2004, using 7 search, September nucleic nucleic . по Run δ

..actggggcctacagctttg tcaaactggggcctccagaa... 0 Н Gapext US-09-801-371A-IDENTITY\_NUC • 10.0 Gapop score: table: Title: Perfect sc Sequence: Scoring

43 ū

> residues 2124099041 3373863 segs, Searched:

6747726 parameters chosen hits satisfying <del>Т</del>0 Total number

seq length: 0 seq length: 2000000000 DB DB Minimum Maximum

. 0% . 100% : 45 summaries Match Match first Post-processing: Minimum Maximum Listing

Geneseq\_29Jan04:\*
geneseqn1980s:\*
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geneseqn2001as:\*
geneseqn2001bs:\*
geneseqn2003as:\*
geneseqn2003as:\*
geneseqn2003as:\*  $\mathbf{z}^{\mathsf{I}}$ чии4июгаоц ,......... • • Database

ve a printed, the number of results predicted by chance to have than or equal to the score of the result being deby analysis of the total score distribution. d. No. is the nurere greater thanis derived by a Pred. score and is

# SUMMARIES

|             |         | dҰ    |      |                 |          |                    |
|-------------|---------|-------|------|-----------------|----------|--------------------|
| sult<br>No. | Score   | are.  | _    | Ω               | ID       | escript            |
| i           | 43      | 001   | . 4. | 1               | AAZ99817 | az99817 Cis-ac     |
| 7           | 43      | 00    | 20   | m               | 9981     | az99815 S          |
| m           | 43      | 000   | 0    | ന               | 9981     | 816 Ci             |
| 4           | 43      | 00    | 787  | ~               | 7        | az20979 Human      |
| വ           | 43      | 00    |      |                 | 7007     | an70075 Human an   |
| <b>9</b>    | 43      | 00    | Н    | ~               | 4,       |                    |
| <b>r</b> ~  | 43      | 00    | Н    | <del>(-1</del>  | 9103     | an91035 XhoI - P   |
| œ           | 43      | 00    | 20   | Н               | 007      | an70072 Human an   |
| Ø           | 43      | 00    | 20   | Н               | 9        | an9096             |
| 10          | 43      | 00    | 27   | ٦,              | Ŋ        | an60558 Sequence   |
| 11          | 43      | 100.0 | 1279 | თ               | ADE25716 | 25716 H            |
| 77          | 43      | 00    | 32   | <del></del> 1   | 36       | n60363 Sequenc     |
| ከ           | 43      | 90    | 32   | m               | A3496    | 34963 Human        |
| .⊣<br>4.    | 43      | 90    | 32   | m               | 108      | £2108              |
| 15          | 43      | 90,   | 32   | 7               |          | Z9677              |
| 16          | 43      | 00    | 56   | <b>-</b> -1     | 2,1      | -1                 |
| 17          | 4.<br>E | 00    | S)   | Н               |          | 3                  |
| 18          | 43      | 00    | 5    | rН              | AAN60557 | 7 Se               |
| ٦<br>9      | 43      | 00    | 58   | <b>_</b>        | 483      | 4836 Hu            |
| 70          | 43      | 000   | 60   | <del>, -1</del> | AAN60446 | Aan60446 Sequence  |
| 21          | 43      | 80.   | 0    | 7               | AAT15424 | Aat15424 Human tum |
| 22          | 43      | 00    | φ    | ⊣               | AAN71307 | 0                  |
| 23          | 43      | 00    | 1643 | ~               | AAT31021 | Aat31021 Human tum |

| 195 Hu | 5757     | 53712 Tu | 964 | 3518 | f64375 Human | 5664 Human | 20983 Chimeri | z20984 Chimer | 9005 TNF-alp | x09014 | a40760 Human | 26377 | E63382 Human | 357891 Human | 494  | 0498 | 585   | 4589     | 608  | 57450 | 86  |
|--------|----------|----------|-----|------|--------------|------------|---------------|---------------|--------------|--------|--------------|-------|--------------|--------------|------|------|-------|----------|------|-------|-----|
| σ      | ACC57575 | 5371     | 4,  | 3518 | F6437        | 566        | 22098         | 2098          | 00           | 901    | 4076         | 5377  | 6338         | 5789         | 5494 | 498  | 04585 | AAD45898 | 8098 |       | 186 |
| 9      | ۲        | 7        | 2   | σ    | 7            | ഗ          | N             | N             | N            | 7      | ო            | m     | 7            | 7            | 7    | ω    | 9     | φ        | 4    | വ     | 7   |
| 1643   | 4        | 64       | 64  | 4,   | 65           | 1666       | 27            | 57            | ന            | 63     | 63           | 63    | 63           | 9            | 63   |      | 91    | φ        | 11   | H     | H   |
| 00     | 100.0    | 00       | 00  | 00   | 00           | 00         | 00            | 00            | 00           | 00     | 00           | 00    | 00           | 00           | 00   | 00   | 00    | 00       | 00   | 00    | 00  |
| 43     | 43       | 43       | 43  | 43   | 43           | 43         | 43            | 43            | 43           | 43     | 43           | 43    | 43           | 43           | 43   | 43   | 43    | 43       | 43   | 43    | 43  |
| 24     | 25       | 26       | 27  | 2.8  | 29           | 30         | 31            | 32            | 33           | 34     | 35           | 36    | 3.7          | 38           | ტ    | 40   | 41    | 42       | 43   | 44    | 45  |

# ALIGNMENTS

Cis-acting nucleotide sequence derived from human TNF-alpha ВР 43 entry) AAZ99817 standard; RNA; (first 12-JUL-2000 AAZ99817; AAZ99817
ID AAZ9
XX
AX
AAZ99817
XX
AX
DE AAZ9
XX
DE CisXX
CisCC Cape
CC Cape
CC CisCC Ci

Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit; RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha; tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

sapiens. Homo WO200014255-A1.

16-MAR-2000

981L-00126112. 981L-00126757. 99WO-IL000483 06-SEP-1999; 07-SEP-1998; 26-OCT-1998;

& DEV CO. (YISS ) YISSUM RES

Ben-Asouli Jarrous N, EL, Osman Kaempfer R,

WPI; 2000-257000/22.

Regulation of gene expression by mRNA splicing is carried out using a cacting nucleotide sequence controlled by phosphorylation of the alphasubunit of eukaryotic initiation factor 2.

75pp; English Claim 5; Page 15; The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders

, structural . The quence can | sensitive to the The sequence can of the splicing of precursor transcripts encoded by that gene sensitiveled of RNA-activated protein kinase (PKR) activity. The sequeused to transform host cells to regulate gene expression at the splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, protein) or industrially or agriculturally applicable protein. present sequence represents a cis-acting nucleotide sequence of invention 

Other; 0 u; T; 0 ወ ö C; 11 A; 13 BP; 10 43 Sequence

Gaps 0 43; Indels Length Score 43; DB 3; 1 Pred. No. 3.1e-07; Mismatches 0; , 0 th 100.0%; Similarity 100.0%; 43; Conservative ( Query Match Best Local S Matches 43

43 43 CTCACTGGGGCCTACAGCTTTGA TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA CAAACTGGGGCCTCCAGAA Н

ESULT

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8

ВР 50 standard; RNA; AAZ99815 AAZ998

AAZ99815; 

entry) (first 12-JUL-2000 necrosis factor-alpha gen of tumour stem loop the ¥ 0 Sequence alpha-subunit : 2; eIF2alpha Cis-acting sequence, intron removal, trans-acting factor; and sectivated protein kinase; eukaryotic initiation factor tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

sapiens Homo

WO200014255-A1

16-MAR-2000

99WO-IL000483 06-SEP-1999; 98IL-00126112 98IL-00126757 07-SEP-1998; 26-OCT-1998;

ပ္ပ DEV پى YISSUM RES ~ (YISS × Ben-Asouli z Jarrous Œ, Osman ಧ Kaempfer

2000-257000/22 WPI;

the alphaout splicing is carried by phosphorylation r 2. of gene expression by mRNA sgleotide sequence controlled beukaryotic initiation factor non of gene e nucleotide s Regulation -acting subunit

English 12pp; 5В; ъ. Ч. 7; Example

guence which is
cencoded by a gene
suce. This removal
and depends on structural The f the human gene renders itive to the equence can be the mRNA TNF-alpha yotic ucleotide protein The specification describes a cis-acting nucleotide sequence which capable of removing introns from a precursor transcript encoded by which harbours at least one cis-acting nucleotide sequence. This rise effected during the production of mRNA of the gene, and depends activation of a trans-acting factor which is an RNA-activated proticinitiation factor 2 (eIP2alpha). Insertion of a cis-acting nucleot sequence, derived from the 3' untranslated region (3'UTR) of the hittmour necrosis factor alpha (TNF-alpha) gene, into another gene resplicing of precursor transcripts encoded by that gene sensitive to splicing of precursor transcripts encoded by that gene sensitive to splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, struction) or industrially or agriculturally applicable protein. The present sequence represents a fragment of the 3'UTR of human TNF-a

Other; 0 ťp **H** 0 T; ö C; 12 A; 15 12 Sequence 50 BP;

ô 50% Indels Length ..0 DB 3; Pred. No. J. 9; Mismatches 43; Score 6 th Similarity 79.1%; 134; Conservative 9 Query Match Local Best Loc Matches

ö

Gaps

47 

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RESULT 3 AAZ99816 ID AAZ99816 standard; RNA; 104

ВР

AAZ99816;

(first entry) 12-JUL-2000 Cis-acting nucleotide sequence derived from human TNF-alpha.

Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit; RNA-activated protein kinase; eukaryotic initiation factor 2; elF2alpha; tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

Homo sapiens

WO200014255-A1

16-MAR-2000.

99WO-IL000483 06-SEP-1999; 98IL-00126112 98IL-00126757 07-SEP-1998; 26-OCT-1998;

ဗ & DEV (YISS ) YISSUM RES Ben-Asouli z Jarrous Osman F, Kaempfer R,

WPI; 2000-257000/22.

Regulation of gene expression by mRNA splicing is carried out using a eacting nucleotide sequence controlled by phosphorylation of the alphasubunit of eukaryotic initiation factor 2.

Claim 4; Page 15; 75pp; English.

The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumourn necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the splicing of precursor transcripts encoded by that gene sensitive to the used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant the mRNA protein) or industrially or agriculturally applicable protein. The present sequence represents a cis-acting nucleotide sequence of the 

Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 U; 0 Other;

Gaps .; 0 Length 104; Indels 100.0%; Score 43; DB 3; 3 100.0%; Pred. No. 3.5e-07; ive 0; Mismatches 0; Conservative Query Match Best Local Similarity Matches 43; Conser

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fragment

Human anti-tumor polypeptide Xho-PstI

(revised)
(first entry)

25-MAR-2003 20-JAN-1991

AAN70075;

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81

DNA;

standard;

AAN70075

cytotoxic;

cancer;

Anti-tumor;

Homo sapiens

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This sequence represents a human TNFalpha (tumour necrosis factor alpha)

3.UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were
constructed comprising at least one TNFalpha promoter enhancer region

(AAZ20975-Z20978), a TNFalpha promoter (AAZ20972-Z20974), a DNA encoding
the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNFalpha

3.UTR sequence. TNFalpha is one of a number of cytokines produced by
inflammatory cells. Upregulation and/or dysregulation of cytokines in
confidence in the apoptosis in the chronic inflammatory diseases. Introduction of the
inflammatory cells. Operating inflammatory diseases them to
connect nucleotide to activated inflammatory cells causes them to
connect nucleotide to activated inflammatory cells causes them to
connect nucleotide to activated inflammatory diseases. Introduction of the
connection of chronic inflammatory diseases. Introduction of the
connection of chronic inflammatory diseases. Introduction of the
consecutive apoptosis. Pharmaceutical compositions of the chimeric nucleotide
constitution and invasive surgery methods
cheaper long-term relief, in comparison with existing conventional
conventional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TNF)
                                                                                                                                                                                                                                                         TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation; chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis; psoriasis; graft versus host disease; lupus erythematosus; diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ч
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A chimeric polynucleotide consisting of a tissue necrosis fact
promoter and an apoptosis-inducing Granzyme B polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G; 221 T; 0 U; 0 Other;
                                  47
   core 43; DB 2;
red. No. 4.9e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOEH ) BOEHRINGER INGELHEIM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barton RW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 100.0%; Similarity 100.0%; 43; Conservative (
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                                                                                                                                                                                            entry)
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                                                                                                                         standard; DNA;
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                                                                                                                                                                                                                             INFalpha 3'UTR
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                                                                                                                                                                                          (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                                                                                                                                                                                                                                                                                                                                       WO9943840-A1.
                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       02-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-1998;
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AAZ20979
ID AAZ20979
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Best Local
                                                                                                                                                          AAZ20979;
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Gaps
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     Length 815
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                                43
                  Indel
                               TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
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     100.0%; Score 43; DB 1; 100.0%; Pred. No. 4.9e-07; ive 0; Mismatches 0;
                                                                                                                                       cell; THP-1; anti-tumour
                  0;
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                                                                                                                                                                                            88JP-00239154
                                                                              817
                                                                                                               entry)
                   Conservative
                                                                             AAQ04340 standard; DNA;
                                                                                                       (revised)
(first en
Query Match
Best Local Similarity
                                                                                                                                         Acute leukaemia
                                                                                                                                                                   JP02088598-A
                                                                                                                                                                                            22-SEP-1988;
                                                                                                                                                      sapiens
                                                                                                                                                                                28-MAR-1990
                                                                                                        25-MAR-2003
21-SEP-1990
                                             716
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                                                                                           AAQ04340
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AAQ0434
ID AA
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Indels

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268

226

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RESULT 5

TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGC

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Best Loc Matches

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The sequence is an Xho-PstI fragment of an anti-tumor protein. The polypeptide is cytotoxic to human tumor cells but not to normal cells. They are also cytotoxic to primary cell cultures obtained from metastasis lesions of patients suffering from striated muscle tumors. They are also resistant to all chemotherapeutic agents. See also AAN70073-74, AAP70077-78 and AAP95592. (Updated on 25-MAR-2003 to correct PR field.)

G; 160 T; 0 U; 0 Other;

C; 205

Sequence 815 BP; 183 A; 267

from

prepd.

DNA

recombinant thp-1.

using

polypeptide(s) - prepd. v of human acute leukaemia

Anti-tumour genomic DNA

WPI; 1987-336540/48

Soma GI;

Mizuno D,

Ü.

(MIZU/) MIZUNO

86JP-00021302. 86JP-00024220. 86JP-00169522.

04-FEB-1986; 07-FEB-1986; 17-JUL-1986;

87EP-00400261

04-FEB-1987

02-DEC-1987

EP247906-A.

Disclosure, Fig 7; 63pp; English

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ВР

1200

DNA;

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The polypeptide is cytotoxic to human tumor cells but not to normal cells. They are also cytotoxic to primary cell cultures obtained from metastasis lesions of patients suffering from striated muscle tumors. They are also resistant to all chemotherapeutic agents. See also AAN70073-75, AAP70077-78 and AAP95592. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-tumour polypeptide(s) - prepd. using genomic DNA of human acute leukaemia cell
                                                                                                                                                                                                                                                                                                                                                                                       4; 63pp; English
                                                                                                       cytotoxic;
                                                                                                                                                                                                                            86JP-00021302.
86JP-00024220.
86JP-00169522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1200 BP; 278 A; 329
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Local Similarity 100.0%;
es 43; Conservative (
                                                                                  Human anti-tumor polypeptide
                                                                                                                                                                                                     87EP-00400261
                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
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                                                                                                         cancer;
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standard;
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                                                                                                                                                                                                                                                                                                                                                                                      Fig
                                                                                                                                                                                                                                                                             (MIZU/) MIZUNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP01095784-A
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25-MAR-2003
11-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells.
                                                                                                                                 sapiens
                                                                                                                                                                                                                            04-FEB-1986;
07-FEB-1986;
17-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                             25-MAR-2003
20-JAN-1991
                                                                                                       Anti-tumor;
                                                                                                                                                                               02-DEC-1987
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                                                                                                                                                        EP247906-A.
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AAN90969
ID AAN90969
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Best Local S
Matches 43
                       AAN70072;
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AAN70072
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                                                                                                                                  003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Section of gene for anticarcinogenic peptide. It is genomic DNA from THP-1 cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                              Used in the prodn. of TNF prodn. agents. (Updated on 25-MAR-2 correct PD field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as anticarcinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 818;
                                                                      and
                                                                                                                                                                                           Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 U; 0 Other;
                                                                                                                                                                    Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                   Indels
                                                                      contain primer
                                                                                                                                                                                                                                          Anticarcinogenic agent; anti-cancer agent; THP-1 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       section of gene for anti-cancer peptide
                                                                                                                                                                                        Score 43; DB 2; Le
Pred. No. 4.9e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 43; DB 1; I larity 100.0%; Pred. No. 4.9e-07; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 818 BP; 184 A; 268 C; 206 G; 160 T;
                                                                      Intrinsic TNF prodn. derivation agents
least one of which has TNF activity.
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                                                                                                          Disclosure; Page ?; 26pp; Japanese.
                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; P
Matches 43; Conservative 0;
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22-SEP-1988;
                        (SOMA/) SOMA
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AAN91035
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                                                         anti-cancer peptide
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                      standard; DNA;
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Score 43; DB 1; I Pred. No. 5.2e-07; Mismatches 0;

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Pred. No. 5.2e-07;
Mismatches 0
                                                253 T;
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                                                 329 C; 340
               for anticarcinogenic peptide.
s. (Updated on 25-MAR-2003 to to correct OS field.)
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  Japanese
                                                               th 100.0%; Similarity 100.0%; 43; Conservative 0
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 17pp;
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protein (hTNF) mature human tumour necrosis factor human tumour necrosis factor i retain antitumour activity. Location/Qualifiers 1. .474 /\*tag= a Wang ВЪ standard; DNA; 1275 86WO-US000236 85US-00698939 SDY, S of hand anticancer; 3 v synthetic muteins direct mutagenesis WPI; 1986-225458/34. P-PSDB; AAP60656. (first CORP encoding ĽŠ, Lin CETUS **DAW731** sapiens 14-AUG-1986. 07-FEB-1985; WO8604606-A. 28-JUL-1991, Antitumour; 03-FEB-1986 AAN60558; AAN60558 Sequence U FJ (CEIU ) ဌ Ношо Key 69 AXA

The sequence encoding TNF produced by the promyelocytic leukemia cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in the TNF sequence appears to be involved in disulphide linkages. The patentors claim a novel synthetic mutein of a biologically active hTNF protein, having at least one cysteine residue free from a disulphide link and non-essential to the activity and having at least one of the cysteine

Disclosure; Fig 3a; 47pp; English.

obtd

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The invention relates to a combination comprising several polynucleotides

having any one of 127 sequences (S1) such as the sequence of human

calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4

thydrolase, human cG1-142 protein mRNA, human K+ channel beat 2 subunit

mRNA, etc., and their complements. The cDNAs are differentially expressed

in LPS (lipopolysaccharide)-treated foam cells. Also included are

containing an extended or full length gene from a library of nucleic acid

sequences, an expression vector containing the nucleic acids, a host cell

containing the vector, a purified polypeptide appearing as ADE25750 and

ADE25751, producing a protein by culturing the host cell, and a

composition comprising a purified antibody that specifically binds to the

proteins. The foam cell-expression of one or more

polynucleotides in a sample. The sample is from a subject with

atheroselerosis and comparison with a standard defines early, mid or late

stages of the disorder. The foam cell-expressed nucleic acids are useful

containity a ligand which binds a polynucleotide. The library is chosen

from DNA molecules, peptides, proteins and RNA molecules or compounds to

identify a ligand which binds a polynucleotide. The library is chosen

from DNA molecules, peptides, proteins and RNA molecules or

compounds to identify at least one ligand which specifically binds a

compounds to identify a least one ligand which specifically binds a

protein, for purifying a ligand from a sample for making a antibody. The

foam cell-expressed nucleic acids are useful for diagnosing
                                                                                                                                                                                                                                                                                                                              cell; LPS; lipopolysaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Combination containing several polynucleotide that are differentially expressed in foam cells and complements of the polynucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.
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Length
                                                                                                                                                                                                                                                                                              Human cDNA differentially expressed in foam cells #120
                                                                                   CAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
Score 43; DB 1; 1
Pred. No. 5.2e-07;
; Mismatches 0;
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                 Similarity 100 43; Conservative
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P-PSDB; ADE25778.
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                      expression
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                                                                       Gaps
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cardiovascular disorder. The foam cell-expressed nucleic acid as elements on a microarray which can be used for detecting rapolynucleotide in a sample, diagnosing cardiovascular disease atherosclerosis. The present sequence represents a cDNA whose is upregulated in LPS treated foam cells.
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P-PSDB;
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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, andiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of disease associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating inpeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive fibrosis, pulmonary hypertension, emphysema, chronic obstructive cancinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the carcinomas, and cancers which may metastasise to the lungs, including calcase of deoxyadenosine which activates adenosine receptors causing release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32312 to AAA35312 represent invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1856 (AAA32323 to
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                                                                                                                                                                                                                                                                                                                                                                Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthmarespiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.
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                                                                                                                                                                                                                                                                                                                                SEQ ID NO:2652
1323
                                      Indels
  Length
                                                                          TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
Score 43; DB 1; I
Pred. No. 5.3e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                               related polynucleotide
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                                     ·;
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  100.0%;
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                                                                                                                                                                                                                                                                                                                                   Human adenosine receptor
                    Similarity 100 43; Conservative
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2004 10:55:23 15 Sep Wed

-100-20-

seguence AAA33992) are specifically claimed ONs from the present invent Sequences given in the disclosure of the present invention do up with their corresponding SEQ ID NO: sequences given in the up with listing 8833333

. N.B. match

Other; 0000 Ŧ, 331 ່ວັ 387 C; 308 Ä 298 1324 BP; Sequence

ô Length 1324; Indels Score 43; DB 3; Pred. No. 5.3e-07; Mismatches 0; .. 0 Query Match Best Local S Matches 43

43 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 755

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AAF21085 standard; DNA; 1324 RESULT 14 AAF21085 

AAF21085;

entry) (first 14-MAR-2001

antisense oligonucleotide related sequence Human low adenosine

#2652

matory;
ostatic;
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RDS;
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rejection;
ronchitis; ergy; Low adenosine antisense oligonucleotide; phosphorothioate; all-human; airway disorder; bronchoconstriction; lung inflammation surfactant depletion; respiratory; bronchodilator; antiinflammimunosuppressive; antiasthmatic; analgesic; hypotensive; cyto respiratory obstruction; pulmonary obstruction; impeded respiratory distress syndrome; pain; cystic fibrosis; allergic pulmonary hypertension; emphysema; pulmonary transplantation rehronic obstructive pulmonary disease; pulmonary infection; br . ເນ cancer;

Homo sapiens.

WO200062736-A2

26-OCT-2000.

24-MAR-2000; 2000WO-US008020

99US-0127958P 06-APR-1999;

EAST CAROLINA. J W.

(UYEC-) UNIV (NYCE)

Nyce JW;

WPI; 2000-679539/66

o not trigger ing cancers nich do treatir Low adenosine (A) content antisense oligonucleotides which adenosine receptors during metabolism, useful e.g. for tresand respiratory obstructions.

Disclosure; Page 887; 1592pp; English

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central

nervous system (CNS) and peripheral nervous and non-nervous system peptide receptors, CNS and peripheral nervous and non-nervous system peptides and transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy (ies) and/or bronchoconstriction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary condition, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention and/or

C; 308 G; 331 T; 0 U; 0 Other; A; 387 1324 BP; 298 Sequence

Gaps ö Length 1324; Indels Score 43; DB 3; ; Pred. No. 5.3e-07; 0; Mismatches 0; ö 100.0%; Similarity 100 43; Conservative Query Match Best Local S Matches 43

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43 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 755 d d ð

5779 ABZ96779 RESULT 15 ABZ96779

ВР 1324 standard; DNA;

17-0CT-2003

ABZ96779;

sednence entry) (first Human nucleic acid

Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory; antiallergic; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. 

sapiens Homo WO200285308-A2

31-OCT-2002

2002WO-US013135 23-APR-2002; 2001US-0286137P 24-APR-2001; EPIGENESIS PHARM INC

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Katz ഗ Sandrasagra A, , Shahabuddin ni Y, Sa Tang L, Ľ JW, Nyce JW Miller

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Aguilar

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WPI; 2003-229219/22

ö Pharmaceutical composition for treating ailments associated with imporespiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid ubiquinone

Disclosure; SEQ ID NO 12021; 872pp; English

pharmaceutical composition, which has oligonucleotide antisense to the s' or 3' end genomic flanking regions or regions within 2-10 nucleotides of The invention relates to a novel first active agent comprising an initiation codon, coding region, 5, and 3' intron-exon junctions,

junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention is antiinflammatory, antiallergic, antiasthmatic, hypotensive, and cytostatic activity. The composition may have a immunosuppressive, and cytostatic activity. The composition may have a cuse in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of adenosine or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO cat ftp.wipo.int/pub/published\_pct\_sequences 

0 U; 0 Other; .; 331 .; Ö C; 308 Sequence 1324 BP; 298 A; 387

Gaps Length 1324; Score 43; DB 7; Pred. No. 5.3e-07; Mismatches 0; Query Match Best Local Similarity 100.0%; F Matches 43; Conservative 0;

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797 43 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA Н 셤  $\overset{\circ}{\circ}$ 

08:05:12 2004, Ŕ September 4 secs Search completed: 3

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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd

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| Run on:                               | September 13, 2004, 12:13:03; Search time 159.422 Seconds (without alignments) 1357.126 Million cell updates/sec |
|---------------------------------------|--|
| Title:<br>Perfect score:<br>Sequence: | US-09-801-371A-2<br>43<br>1 tcaaactggggcctccagaaactggggcctacagctttga 43  |
| Scoring table:                        | IDENTITY_NUC<br>Gapop 10.0 , Gapext 1.0  |
| Searched:                             | 3304383 seqs, 2515761380 residues  |
| Total number of hits                  | hits satisfying chosen parameters: 6608766   |

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being print and is derived by analysis of the total score distribution.

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| No             | Score | Query | Length | DB       |                  | BCL             |
|----------------|-------|-------|--------|----------|------------------|-----------------|
| <br> <br> <br> | 433   | 100.0 | ı m    | 1<br>1 O | US-09-801-371A-2 | , Appl          |
| 0              | 43    | 0     | 4.3    | σı       | A                | e 6, Appl       |
| 6)             | 43    | 100.0 | 50     | σι       | -801-37          |                 |
| 4              | 43    | 0     | 87     | σι       | -801-371A-       | nce 7, Appl     |
| ம              | 43    | 0     | 0      | σ        |                  | sence 1, Appl   |
| ω<br>υ         | 43    | 100.0 | 104    | σı       | -371A-           | quence 5, Appl  |
| 7              | 43    | 0     | æ      | 13       | 0                | mence 13, App   |
| 80             | 43    | O     | 27     | 15       | 7-671-12         | equence 120, A  |
| თ              | 43    | O     | œ      | 13       | 0                | equence 501, Ap |
|                | 43    | 0     | 58     | 13       | 2-11             | equence 501, Ap |
|                | 43    | O     | ထ      | 17       | -643-132         | equence 1329, A |
| 12             | 43    | 0     | 4      | 13       |                  | equence 1901, A |
|                | 43    | 0     | 44     | 13       | -118-190         | e 1901, A       |
|                | 43    | 00    | 4      | 15       | US-10-272-411-4  | equence 4, Appl |

| lence 3, Applance 9, Applance 9, Applance 1, Applance 24, Applance 28, Applance 6223, Applance 6223 | р, ооо ооо н н   |
|--|--|
| 5 US-10-218-547-3<br>5 US-10-272-328A-4<br>5 US-10-310-793-9<br>5 US-10-247-671-68<br>3 US-09-973-850-1<br>3 US-09-973-850-3<br>0 US-09-973-850-3<br>0 US-09-973-850-3<br>10S-10-202-062-3<br>6 US-10-191-997-104<br>7 US-10-652-795-1<br>7 US-10-647-918-1<br>6 US-10-429-802-33<br>6 US-10-429-802-33<br>6 US-10-652-696-28<br>7 US-10-622-696-28<br>7 US-10-040-862-6223<br>6 US-10-057-475B-6223<br>6 US-10-057-475B-6223<br>6 US-10-154-884B-6223   | 15 US-10-312-841- 0 US-09-535-459-1 3 US-10-027-632-1 6 US-10-027-632-1 6 US-10-0242-535A- 6 US-10-027-632-1 6 US-10-027-632-1 6 US-10-027-632-1 6 US-10-027-632-1 6 US-10-027-632-1 |
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# ALIGNMENTS

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Gaps
           US-09-801-371A-2

Sequence 2, Application US/09801371A

Sequence 2, Application US/09801371A

Patent No. US20020155569A1

GENERAL INFORMATION:

APPLICANT: Campfer, Raymond

APPLICANT: Osman, Farhat

APPLICANT: Jarrous, Nayef

APPLICANT: Ben-Asouli, Yitzhak

TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH

TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES

FILE REFERENCE: A34084-PCT-USA-A 066031.0147

CURRENT APPLICATION NUMBER: US/09/801,371A

CURRENT APPLICATION NUMBER: PCT WO 00/14255

PRIOR FILING DATE: 1999-09-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 43

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 9; | Pred. No. 8.3e-08; | Mismatches 0;
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43; Conserv
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Best Local S
Matches 43
RESULT 1
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RESULT 2 US-09-801-371A-6/c ; Sequence 6, Application US/09801371A ; Patent No. US20020155569A1

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Sequence 1, Application US/09801371A

Sequence 1, Application US/09801371A

Patent No. US2002015569A1

GENERAL INFORMATION:

APPLICANT: Kaempfer, Raymond

APPLICANT: Osman, Farhat

APPLICANT: Darrous, Nayef

APPLICANT: Ben-Asouli, Yitzhak

TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH

TITLE OF INVENTION: MANIPULATION OF GENE EXPRESSION

TITLE OF INVENTION: MANIPULATION OF GENE APPLICING AND ITS

FILE REFERENCE: A34084-PCT-USA-A 066031.0147

CURRENT APPLICATION NUMBER: US/09/801,371A

CURRENT APPLICATION NUMBER: PCT WO 00/14255

PRIOR FILING DATE: 1999-09-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 104
  FILE REFERENCE: A34084-PCT-USA-A 06
CURRENT APPLICATION NUMBER: US/09/8
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Versi
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-801-371A-1
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Best Local
Matches 3
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; Sequence 8, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; TITLE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09801371A;
Sequence 7, Application US/09801371A;
Patent No. US20020155569A1;
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond;
APPLICANT: Osman, Farhat;
APPLICANT: Jarrous, Nayef;
APPLICANT: Ben-Asouli, Yitzhak;
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH;
TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES;
                                                                                                                                        USES
GENERAL INFORMATION:

APPLICANT: Kaempfer, Raymond
APPLICANT: Osman, Farhat
APPLICANT: Jarrous, Nayef
APPLICANT: Jarrous, Nayef
APPLICANT: Jarrous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USE
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 50;
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Pred. No. 8.3e-08;
0; Mismatches 0;
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8.3e-08;
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Similarity 79.1%;
4; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                            th similarity 100.0%; 43; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-801-371A-8
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SEQ ID NO 8
LENGTH: 50
TYPE: RNA
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Best Local S
Matches 34
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Best Local S
Matches 43
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US-09-8
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Indels

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Score 43; DB 9; Pred. No. 8.3e-08 ; Mismatches

6

th 100.0%; Similarity 79.1%; 34; Conservative 5

ORGANISM: Homo sapien

LENGTH:

-USA-A 066031.01 : US/09/801,371A

TCAAACTGGGGCCTCCAGAA

Length 81;

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                                                                                                                                           us-09-801-371A-5/c

sequence 5, Application US/09801371A

Patent No. US20020155569A1

GENERAL INFORMATION:

APPLICANT: Kaempfer, Raymond

APPLICANT: Osman, Farhat

APPLICANT: Osman, Farhat

APPLICANT: Darrous, Nayef

TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH

TITLE OF INVENTION: MAINIBULATION OF MRNA SPLICING AND ITS

FILE REFERENCE: A34084-PCT-USA-A 066031.0147

CURRENT APPLICATION NUMBER: DCT WO 00/14255

PRIOR APPLICATION NUMBER: PCT WO 00/14255

PRIOR FILING DATE: 1999-09-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Verein.
                                           Indels
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                                                                             DB 9; L
8.3e-08;
         Score 43; DB
Pred. No. 8.3
; Mismatches
                                            ..
0
       th 100.0%; Similarity 100.0%; 43; Conservative (
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          Query Match
Best Local S
Matches 43
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Length 104;

DNA

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1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
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Pred. No. 8.3e-08;
Mismatches 0;
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Pred. No. 8.3e-08;
Mismatches 0;
                                                                                                                                                                  US20030194721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Kao, Mao
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van 't Veer, Marc
; APPLICANT: Van 't Veer, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10342887
5. US20040058340A1
                                                                                                                                                                                                                                                                                                                                         CAAACTGGGGCCTCCAGAACTCA
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Van de Vijver, Marc
Bernards, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 43; Conservative (
                                                                                                                                                                                                                                       100.0%;
larity 100.0%;
Conservative (
                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID
US-10-247-671-120
                                                                                                                                                                                                                                                                                                                                                                                                                                       LESULT 9
US-10-342-88,
; Sequence 501, Ar.
; Publication No. US2v.
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Linsley, Peter S.
TCANT: Roberts, Christc
TTCANT: Roberts, Christc
TTCANT: Roberts, La'
TTCANT: Roberts, Christc
TTCANT: Roberts, Christc
TTCANT: Roberts, Christc
TTCANT: Roberts, La'
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      Program
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Best Local Similarity
Matches 43; Conser
    PERL
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SOFTWARE: PERL
SEQ ID NO 120
LENGTH: 1279
TYPE: DNA
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US-10-247-671-120
; Sequence 120, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; TILE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
                                                                                                                                                   Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inflammatory
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                                                                                                                                                                                                                                                US-10-356-308A-13

US-10-356-308A-13

Sequence 13, Application US/10356308A

Publication No. US20040039186A1

GENERAL INFORMATION:

APPLICANT: Tatake, Revati J.

APPLICANT: Marlin, Steven D.

APPLICANT: Barton, Randall Wilber

TITLE OF INVENTION: Self-Regulated Apoptosis of Inf

TITLE OF INVENTION: Self-Regulated Apoptosis of Inf

CURRENT APPLICATION NUMBER: US/10/356,308A

CURRENT FILING DATE: 1998-02-27

PRIOR FILING DATE: 1998-02-27

PRIOR FILING DATE: 1997-02-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 13

LENGTH: 787
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Pred. No. 8.3e-08;
); Mismatches 0;
                                                                                                                                                Score 43; DB 9; Pred. No. 8.3e-08; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1 to 787

LOCATION: 1 to 787

OTHER INFORMATION: TNFa 3' untrapropertion information:
AUTHORS: Nedwin, G.E., et al.
JOURNAL: Nucleic Acid Research
VOLUME: 13
PAGES: 6361-6373
DATE: 1985
S-10-356-308A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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Similarity 100.0%;
43; Conservative (
                                                                                                                                                 th similarity 100.0%; 43; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                sapien
      EQ ID NO 5
LENGTH: 104
TYPE: DNA
ORGANISM: HOMO
                                                                                    ; US-09-801-371A-5
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Best Local S
Matches 43
                                                                                                                                                    Query Match
Best Local S
Matches 43
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US-10-3
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Cancer Patients

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Gaps

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Length 1279

561301CB1

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Cancer
                           Breast
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-175-999
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Gaps

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1585;

Length

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                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 13;
Pred. No. 8.3e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, IN
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Window
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <UNKNOWN>
FILING DATE: CUNKNOWN>
FILING DATE: CONMUNICATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 845-0555
TELEPHONE: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE
CURRENT APPLICATION NUMBER: US/10/172,118

CURRENT FILING DATE: 2002-06-14

PRIOR APPLICATION NUMBER: 60/380,770

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 2699

SEQ ID NO 501

LENGTH: 1585

TYPE: DNA

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: NM 000594

DATABASE ENTRY DATE: 2001-06-18

US-10-172-118-501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Seilhamer
F INVENTION: COMPOSITION FOR T
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-10-641-643-1329
; Sequence 1329, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1329:
SEQUENCE CHARACTERISTICS:
LENGTH: 1585 base pair:
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                          ;
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CLONE: 9339737
SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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1585

Length

17;

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43;

Score

100.0%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1074 TCAAACTGGGGCTCCAGAACTCACTGGGGGCCTACAGCTTTGA
1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGGCCTACAGCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                     Breast
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Pred. No. 8.3e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-10-172-118-1901
; Sequence 1901, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Wan 't Veer, Laura
; APPLICANT: Wan 't Veer, Laura
; APPLICANT: Wan 't Veer, Laura
; APPLICANT: Wan de Vijver, Marc
; APPLICANT: Wan de Vijver, Marc
; APPLICANT: Unwention: Diagnosis and Prognosis of
; TITLE OF INVENTION: Diagnosis and Prognosis of
; FILE RFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1901
; LENGTH: 1643
; TYPE: NNA
                                                                           US-10-342-887-1901
Sequence 1901, Application US/10342887
Sequence 1901, Application US/10342887
Bublication No. US20040058340A1
GENERAL INFORMATION:
APPLICANT: He, Yudong
APPLICANT: He, Yudong
APPLICANT: Hao, Mao
APPLICANT: Mao, Mao
APPLICANT: Wan 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Un de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1901
LENGTH: 1643
TAVDE: NATA
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: X01394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 100.0%; Similarity 100.0%; 43; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-10-342-887-1901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 43
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Gaps

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Pred. No. 8.3e-08 Mismatches 0

Similarity 100.0%; I 43; Conservative 0;

Best Local Matches

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43

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1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: September 13, 2004, 16:11:26 Job time: 161.422 secs
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SEQ ID NO 3
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-218-547-3
                                                                                                                                                                                                                                th 100.0%;
Similarity 100.0%;
43; Conservative (
                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-10-218-547-3
; Sequence 3, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel;
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
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Pred. No. 8.3e-08;
; Mismatches 0;
                                                                        Score 43; DB 13;
Pred. No. 8.3e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                      RESULT 14
US-10-272-411-4
US-10-272-411-4
US-10-272-411-4
US-10-272-411-4
Sequence 4, Application US/10272411
Sequence 4, Application No. US20030100068A1
GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREO;
FILE REFERENCE: 6019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
CURRENT APPLICATION NUMBER: 60/329,393
PRIOR PILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/329,393
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 4
LENGTH: 1643
TYPE: DAT
ORGANISM: HOMO SADIENS
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1995-03-21
RELEVANT RESIDUES: (1)...(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)...(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)...(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)...(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-08
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-08
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)...(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-08
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)...(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-08
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)...(1643)
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       2001-06-18
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Best Local Similarity 100.0%;
Matches 43; Conservative 0
                                                                        th 100.0%; Similarity 100.0%; 43; Conservative (
          DATE:
         ; DATABASE ENTRY
US-10-172-118-1901
                                                                          y Match
Local 8
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Best Loc
Matches
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Length 1643;

Score 43; DB 15; Pred. No. 8.3e-08; Mismatches 0;

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US-09-801-371Ascore: Title: Perfect

tcaaactggggcctccagaa... Sequence:

IDENTITY NUC Gapop 10.0, table: Scoring

residues 682709 seqs, 277475446 Searched:

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Gapext

 $\boldsymbol{\omega}$ 136541 parameters: chosen satisfying hits o O number Total

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2000000000 length: length: seq seq Minimum Maximum

0% 100% 45 summaries Post-processing: Minimum Match Maximum Match Listing first

sued Patents NA:\*
/cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\* H .. .. .. .. **പ**им 4 50 40 Databas

/e a printed, . No. is the number of results predicted by chance to have greater than or equal to the score of the result being is derived by analysis of the total score distribution. Pred. N score g and is

#### SUMMARIES

| Description         | equence 13, Ap  | equence 7, Appl | equence 1329, A | equence 36, App | equence 4, Appl | equence 13, App | equence 14, App | equence 1, Appl | equence 1, Appl | equence 34, App | equence 72, App | equence 126, Ap | equence 3, Appl | equence 1, Appl | equence 3, Appl | equence 5, Appl | equence 978, Ap | equence 2765, A | equence 714, Ap | equence 551, Ap | equence 1, Appl   | equence 1, Appl | equence 1, Appl       | equence 1, Appl | equence 1, Appl       | ence 1, Appl | equence 1, Appl |
|---------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-------------------|-----------------|-----------------------|-----------------|-----------------------|--------------|-----------------|
| ID                  | US-09-032-297A- | -09-229-15      | 5-09-023-655-1  | 5-08-880-342-3  | S-09-505-250-   | S-09-229-151    | -09-229-151C-1  | S-09-166-186-   | 8-09-313-93     | 5-09-109-663-3  | S-09-148-545-   | S-09-148-545-1  | S-09-740-027-   | CT-US95-12987-  | CT-US95-12987-  | T-US95-12987-   | S-09-621-976-97 | 8-09-621-976-27 | S-09-621-976-7  | 8-09-833-381-55 | -409-731          | -08-470-298B-   | S-09-023-073A-        | 18-09-361-737-  | -08-820-825-          | -60-         | -09-734-036-    |
| B (                 | 4               | 4               | 4               | ო               | 4               | 4               | 4               | m               | ო               | m               | 4               | 4               | 4,              | rv.             | ហ               | ហ               | 4               | 4               | 41              | 4               | н                 | ~               | 7                     | ო               | N                     | ო            | 4               |
| Length              | 787             | $\mathbf{m}$    | 53<br>89        | 64              | 64              | 27              | <u></u>         | 63              | 63              | 63              | 27              | 29              | 70              | <u></u>         | <u></u>         | _               | Φ               | 0               | m               | ഗ               | Q                 | Q               | Ø                     | v               | 4                     | 944          | 4               |
| %<br>Query<br>Match | 100             | O               | $\mathbf{O}$    | $\mathbf{o}$    | О               | 0               | 100.0           | 0               | Ф               | 00              | σ               | σ               | 9               | 48.8            | ω               | 48.8            | ω               | α               | 48.4            | $\infty$        | $\mathbf{\omega}$ | ത               | $\boldsymbol{\omega}$ | 48.4            | $\boldsymbol{\omega}$ | 48.4         | α               |
| Score               | 4.              | 43              | 43              | 4.3             | 43              | 43              | 4.              | 43              | 43              | 43              | H               | 21,4            | Η.              | 21              | 21              | Ŋ               | Ö               | ö               | ö               | ö               | ö                 | Ö               | Ö                     | Ö               | ö                     | 20.8         | Ö               |
| Result<br>No.       | ત               | C)              | ო               | 4,              | ιΩ              | 9               | 7               | ω               | o               | 10              | <u>ц</u>        | υ<br>17         | 13              | 14              | 15              | 16              | 17              | 18              | 19              | c 20            | 21                | 22              | 23                    | 24              | 25                    | 26           | 27              |

| quence 2, Ap<br>quence 3, Ap<br>quence 32, Ap<br>quence 212,<br>quence 212,<br>quence 212,<br>quence 214,<br>quence 214,<br>quence 214,<br>quence 354,<br>quence 354,<br>quence 354,<br>quence 354,<br>quence 361,<br>quence 361,<br>quence 361, | ednemce i, Appr |
|--|-----------------|
|  | 48+             |
| - M 44 44 M M M M M M M M M M M M M M M  | 4               |
| 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0  | -               |
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| 00000000000000044444<br>8000100450000010041  | 45              |
| 0 0000000000000  | U               |

# ALIGNMENTS

Therapy Steven D. Marlin and Corporation Box 368 of Gene d Apoptosis Cells by Ger ; sequence description: SEQ ID NO: 13: US-09-032-297A-13 INLIAMMMATORY CELIES DY

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: Boehringer Ingelheim Corpoi
STREET: 900 Ridgebury Road, P.O. Box:
CITY: Ridgefield
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06877-0368

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER READABLE FORM:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 00/038,266
FILING DATE: 28-FEB-97
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 25089
REFERENCE/DOCKET NUMBER: 25089
REGUENCE CHARACTERISTICS:
LEMOTH: 787
TYPE: MUCIET ACIM Sequence 13, Application US/09032297A
Patent No. 6525184
GENERAL INFORMATION:
APPLICANT: Revati J. Tatake, Stever
Randall W. Barton
TITLE OF INVENTION: Self-Regulated
Inflammatory Ce RESULT 1 US-09-032-297A-13

787; Length DB 4; I Score Pred. 1 100.0%; Query Match Best Local Similarity

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REGISTRATION NUMBER
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43; Conserv
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Best Local S
Matches 43
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  Indels
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US-09-023-655-1329

Sequence 1329, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
VIMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
COUNTRY: USA
INFOLMARE: Word Perfect 6.1 for Windows/MS-DOS
CORPATING SYSTEM: PC-DOS/MS-DOS
CONPUTER: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
                               9
                                                                                                      RESULT 2
US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inf;
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 43; Conservative 0; Mismatches 0;
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0
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ORGANISM: Human
FEATURE:
OTHER INFORMATION: TNF-alpha untranslated region
09-229-151C-7
  Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
  Conservative
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LENGTH: 787
  43;
  Matches
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US-09-023
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US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
                                                 Length 2270;
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                                                                                                                                                                                                                                                                                                                          Inflammatory
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                                                                                                                                1709 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
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  -706TNFpGB3'UTR
                                                Score 43; DB 4;
Pred. No. 2.1e-08;
Mismatches 0;
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Pred. No. 2.1e-08;
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                                                                                                                                                                                                                    Sequence 14, Application US/09229151C

Patent No. 6537784

GENERAL INFORMATION:

APPLICANT: Tatake, Revati J.

APPLICANT: Marlin, Steven D.

APPLICANT: Barton, Randall W.

TITLE OF INVENTION: Self-Regulated Apoptosis of FILE REFERENCE: 9/137

CURRENT APPLICATION NUMBER: US/09/229,151C

CURRENT FILING DATE: 1999-01-12

PRIOR FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 2.0

SEQ ID NO 14

LENGTH: 2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS (796..981,1589..1634,1822..1869,2171
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100.0%; P3
; OTHER INFORMATION: chimeric gene US-09-229-151C-13
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                                              th 100.0%;
Similarity 100.0%;
43; Conservative (
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Best Local Similarity 100
Matches 43; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (796..981,1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .. (1588)
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; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: C
US-09-229-151C-14
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(982)..
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(615)
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                                                Query Match
Best Local S
Matches 43
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Rao, Peter
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1643
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                                                                TNF cDNA HSTNFR (EMBL Accession #X01394)
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                                                                                                                                                                                                                                            1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
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Pred. No. 1.9e-08; ; Mismatches 0;
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Pred. No. 1.9e-08;
0; Mismatches 0;
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US-09-229-151C-13

Sequence 13, Application US/09229151C

Patent No. 6537784

GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Marlin, Steven D.
APPLICANT: Barton, Randall W.
TITLE OF INVENTION: Self-Regulated Apoptosis of FILE REFERENCE: 9/137
CURRENT APPLICATION NUMBER: US/09/229,151C
CURRENT FILING DATE: 1999-01-12
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 2.0
SEQ ID NO 13
LENGTH: 2270
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Best Local Similarity 100.0%;
Matches 43; Conservative (
     (genomic)
                                                                                                                                                                                            Similarity 100
43; Conservative
MOLECULE TYPE: DNA (96
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

; NAME/KEY: CDS

; LOCATION: (153)...(854)

US-09-505-250-4
                                                                                                                CDS
153..851
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ORGANISM: Human
FEATURE:
    HYPOTHETICAL
HYPOTHETICAL
HYPOTHETICAL
ANTI-SENSE:
ORIGINAL SOUF
INDIVIDUAL
INDIVIDUAL
HEATURE:
HEATURE:
NAME/KEY:
LOCATION:
US-08-880-342-36
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Best Local
Matches 4
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Sequence 34, Application US/09109663

Sequence 34, Application US/09109663

Patent No. 6277981

GENERAL INFORMATION:

APPLICANT: Tu, Guang-Chou

APPLICANT: Israel, Yedy

TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF

TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF

TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF

TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF

TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF

TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF

TITLE OF INVENTION NUMBER: US/09/109,663

CURRENT FILING DATE: 1998-07-03

HOWBER OF SEQ ID NOS: 81

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3634;
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Pred. No. 2.2e-08;
; Mismatches 0;
                                                                                                                                                                                         NAME/KEY: exon
LOCATION: (2171)..(3381)
FUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Smith, D.
AUTHORS: Pennica, D.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis for TITLE: structure, homology and chromosomal locations.
COURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATE: 1985-09-11

DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: TNF(alpha) cDNA US-09-109-663-34
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.larity 100.0%;
.Conservative 0;
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Best Local Similarity 100.
Matches 43; Conservative
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(1822)..(1869)
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LENGTH: 3634
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
  (1589)..(1634)
                                                       .. (1821)
                                                                                                                                              intron
(1870)..(2070)
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43; Conserv
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(1635).
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US-09-109-663-34
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Best Local S
Matches 43
  LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
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FEATURE:
NAME/KEY:
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                                                                                                                                                                                                       NAME/KEY: exon
LOCATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Smith, D.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor genes: str
TITLE: homology and chromosomal localization
JOURNAL: Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE ENTRY DATE: 1997-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
(796..981,1589..1634,1822
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Best Local Similarity 100.0%;
Matches 43; Conservative 0;
    exon
(1589)..(1634)
                                                                                                           excn (1822)..(1869)
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(982)..(1588)
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(1870)
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(1635)
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LENGTH: 3634
TYPE: DNA
ORGANISM: HOMO S
FEATURE:
NAME/KEY: CDS
LOCATION: (796...
FEATURE:
NAME/KEY: exon
LOCATION: (615).
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LOCATION:
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                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2812
NAME/KEY:
LOCATION:
FEATURE:
                                         FEATURE:
NAME/KEY:
LOCATION:
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RESULT US-09-3

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BARLIER FILING DATE: 1997-05-23
BARLIER APPLICATION NUMBER: 60/043,568
BARLIER APPLICATION NUMBER: 60/043,568
BARLIER APPLICATION NUMBER: 60/043,568
BARLIER PILING DATE: 1997-04-11
BARLIER PILING DATE: 1997-04-11
BARLIER FILING DATE: 1997-04-11
BARLIER FILING DATE: 1997-04-11
BARLIER FILING DATE: 1997-04-11
BARLIER FILING DATE: 1997-04-11
BARLIER PILING DATE: 1997-06-22
BARLIER P
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APPLICANT: Rosen et al.

TITLE OF INVENTION: 70 Human Secreted Protein
FILE REFRENCE: POOLD!

CURRENT PLING DATE: 1999 09-04
EARLIER PLING DATE: 1999 09-04
EARLIER APPLICATION NUMBER: UG/040,162
EARLIER APPLICATION NUMBER: UG/040,162
EARLIER APPLICATION NUMBER: CG/040,133
EARLIER PLING DATE: 1997 03-07
EARLIER APPLICATION NUMBER: CG/040,333
EARLIER PLING DATE: 1997 03-07
EARLIER APPLICATION NUMBER: CG/040,052
EARLIER FILING DATE: 1997 03-07
EARLIER APPLICATION NUMBER: CG/040,533
EARLIER APPLICATION NUMBER: CG/040,533
EARLIER APPLICATION NUMBER: CG/047,503
EARLIER APPLICATION NUMBER: CG/047,503
EARLIER APPLICATION NUMBER: CG/047,503
EARLIER FILING DATE: 1997 05-23
EARLIER FILING DATE: 1997 05-23
EARLIER PLING DATE: 1997 05-
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Pred. No. 12;
0; Mismatches
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EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 19
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5-09-148-545-126/c
Sequence 126, Application US/0914854!
Patent No. 6590075
GENERAL INFORMATION:
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Best Local Similarity 80.6%;
Matches 25; Conservative
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RESULT US-09-1

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RAPELICATION NUMBER: 60/043,569

EX FILING DATE: 1997-04-11

EX PELING DATE: 1997-04-12

EX PELING DATE: 1997-04-12

EX PELING DATE: 1997-04-12

EX PELING DATE: 1997-04-12

EX PELING DATE: 1997-08-22

EX PELING DATE: 1997-08-2 EARLIER

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TRANSPORTER
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US-09-740-027-3
Sequence 3, Application US/09740027
Sequence 3, Application US/09740027
Batent No. 6485939
JENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: COFACTOR PROTEINS, AND USES THEREOF
TITLE OF INVENTION: COFACTOR PROTEINS, AND USES THEREOF
TITLE OF INVENTION: US/09/740,027
CURRENT FILING DATE: 2000-12-20
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Pred. No. 12;
0; Mismatches
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER PELICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-06-23
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EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-08-22
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Best Local Similarity 80.6
Matches 25; Conservative
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GENERAL INFORMATION:
APPLICANT: LAFEMINA, R.
APPLICANT: LAFEMINA, R.
APPLICANT: SARDARA, V.
APPLICANT: SARDARA, V.
APPLICANT: SARDARA, V.
APPLICANT: SARDARA, V.
APPLICANT: VELOSKI, C.
TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
NUMBER OF SEQUENCES:
ADDRESSEE: ROY D. MEREDITH
STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
CITY: RAHWAY.
STATE: NEW JERSEY
COUNTRY: USA
ZIP: NEW JERSEY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
COMPUTER: Patentin Release #1.0, Version #
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Pred. No. 21
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SEQ ID NOS: 4
FastSEQ for Windows Version
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PCT-US95-12987-3
Sequence 3, Application PC/TUS9512987
GENERAL INFORMATION:
APPLICANT: LAFEMINA, R.
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llarity 73.0%;
Conservative
                                                                                                                                                                                               th 49.8%; Similarity 80.6%; 25; Conservative
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STRANDEDNESS: acceptology: linear
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                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-09-740-027-3
NUMBER OF SEQ I
SOFTWARE: FastS
SEQ ID NO 3
LENGTH: 24707
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PCT-US95-12987-1
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                                                                                                                                                                                                Query Match
Best Local S
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PCT-US95-1
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APPLICANT: SARDANA, V.
APPLICANT: VELOSKI, C.
TITLE OF INTENTION: STABLE RECOMBINANT HOWV PROTEASE
NUMBER OF SEQUENCES:
ADDESSES: ROY D. MEREDITH
STATE: NUM JERSEY
COMPUTER: NUM JERSEY
STATE: NUM JERSEY
STATE: NUM JERSEY
COMPUTER: REDABLE PORM:
MUSH OF SCHOOL 126 E. LINCOLN AVE.
STATE: NUM JERSEY
COMPUTER: REDABLE PORM:
MUSH OF SCHOOL 126 E. LINCOLN AVE.
STATE: NUM JERSEY
COMPUTER: NUM JERSEY
COMPUTER: SELVENCE COMPATION
MUSHER TARENT APPLICATION NUMBER: PCT/US95/12987
CLASSIFICATION NUMBER: PCT/US95/12987
CLASSIFICATION NUMBER: PCT/US95/12987
CLASSIFICATION NUMBER: 30,777
REFERENCE CHARACTERS 130,777
REPRENCE CHARACTERS 130,777
RELECONOMICATION NURORATION:
NUME: NEEDENCE (908) 594-4678
TELEFOX: (908) 594-4678
TELEFO
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being printed
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cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*

cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

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cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*

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cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

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US-10-172-118-501

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US-10-172-118-1901

US-10-272-411-4

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Sequence 2, Applia Sequence 1, Applia Sequence 24, Applia Sequence 24, Applia Sequence 24, Applia Sequence 2, Applia Sequence 2, Applia Sequence 2, Applia Sequence 6, Applia Sequence 6, Applia Sequence 6, Applia Sequence 6, Applia Sequence 6223, Applia Sequence 6223, Applia Sequence 6223, Applia Sequence 10, Applia Sequence 1463, Applia Sequence 1141, Applia Sequence 12, Applia Sequence 1463, Applia Sequence 120, Applia Sequence 2207, Applia Sequence 22007, Applia Ap
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US-09-801-371A-1

US-09-801-371A-1

Sequence 1, Application US/09801371A

Patent No. US20020155569A1

GENERAL INFORMATION:

APPLICANT: Kaempfer, Raymond

APPLICANT: Osman, Farhat

APPLICANT: Osman, Farhat

APPLICANT: Osman, Farhat

TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH

TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS US

FILE REFERENCE: A34084-PCT-USA-A 066031.0147

CURRENT FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: PCT WO 00/14255

PRIOR APPLICATION NUMBER: PCT WO 00/14255

PRIOR FILING DATE: 1999-09-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

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13 US-09-973-850-3
10 US-09-824-322B-1
10 US-09-932-300-34
13 US-10-202-062-3
16 US-10-191-997-104
17 US-10-652-795-1
16 US-10-429-802-33
16 US-10-429-802-33
15 US-10-429-802-33
15 US-10-312-841-2
15 US-09-801-371A-8
15 US-09-801-371A-8
15 US-09-801-371A-6
15 US-09-801-371A-6
15 US-09-801-371A-6
15 US-09-801-371A-6
15 US-10-312-841-1
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15 US-10-292-799-60620
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Pred. No. 7.2e-28
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Matches 104; Conservat
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Best Local Similarity 100
Matches 104; Conservative
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US-10-342-887-501
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RESULT 2
US-09-801-371A-5/c
Sequence 5, Application US/09801371A
Fatent No. US20020155569A1
FAPLICANT: Raymond
APPLICANT: Jarrous, Nayef
APPLICANT: Jarrous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
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Pred. No. 7.2e-28;
Mismatches 0;
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Pred. No. 1e-27;
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LOCATION: 1 to 787

LOCATION: 1 to 787

OTHER INFORMATION: TNFa 3' untranslated region
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E., et al.
JOURNAL: Nucleic Acid Research
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-US-10-356-308A-13

-US-10-356-308A-13

Sequence 13, Application US/10356308A

Publication No. US20040039186A1

GENERAL INFORMATION:

APPLICANT: Tatake, Revati J.

APPLICANT: Marlin, Steven D.

APPLICANT: Barton, Randall Wilber

TITLE OF INVENTION: Self-Regulated Apoptosis

FILE REFERENCE: 9/121-1-CIP1

CURRENT APPLICATION NUMBER: US/10/356,308A

CURRENT FILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: US 60/039,266

PRIOR FILING DATE: 1998-02-27

PRIOR FILING DATE: 1998-02-27

PRIOR FILING DATE: 1997-02-28

NUMBER OF SEQ ID NOS: 13

LENGTH: 787

TYPE: DNA

TYPE: DNA
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Matches 104; Conservative (
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Best Local Similarity
Matches 104; Conser
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Pred. No. 1.1e-27;
; Mismatches 0;
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Sequence 501, Application US/10342887

Publication No. US20040058340A1

GENERAL INFORMATION:

APPLICANT: Dai, Hongyue

APPLICANT: Mao, Mao

APPLICANT: Mao, Mao, Mac

APPLICANT: Wan 't Veer, Laura Johanna

APPLICANT: Van 't Veer, Laura Johanna

APPLICANT: Wan 't Veer, Laura Johanna

APPLICANT: WUMBER: US/10/342,887

CURRENT APPLICATION NUMBER: 60/298,918

PRIOR FILING DATE: 2001-06-18

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 2699

NUMBER OF SEQ ID NOS: 2699

MANDER DE LENGEN APPLICATION NUMBER: LOFITAL APPLICANTION NUMBER: LOFITAL APPLI
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Sequence 501, Application US/10172118
Publication No. US20030224374A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: Linsley, Peter
APPLICANT: Linsley, Peter
APPLICANT: Wao, Mao
APPLICANT: Woer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Usher)
APPLICANT: Usher, Laura
APPLICANT: Usher, Laura
APPLICANT: Usher, Laura
APPLICANT: Usher, Marc
APPLICANT: Usher, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 2699
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                                                                                                                                                                                                                  Score 104; DB 13;
Pred. No. 1.1e-27;
0; Mismatches 0;
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NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INSTREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER: ISA
COMPUTER: 
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US-10-641-643-1329
; Sequence 1329, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
Jeffrey J. Seilhamer
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . H
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No.
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: HOMO SADIENS
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 000594
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-501
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Best Local Similarity 100.0%;
Matches 104; Conservative
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CLONE: 9339737
SEQUENCE DESCRIPTION:
-10-641-643-1329
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Pred. No. 1.1e-27;
0; Mismatches 0;
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US-10-342-887-1901

Sequence 1901, Application US/10342887

Publication No. US20040058340A1

GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: He, Yudong
APPLICANT: Mao, Mao
APPLICANT: Wan 't Veer, Laura Johanna
APPLICANT: Wan 't Veer, Laura Johanna
APPLICANT: Wan de Vijver, Marc J.
APPLICANT: Wan de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1901

LENGTH: 1643

TUPE: NAA
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; Sequence 1901, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Nan, Mac, Marc
; APPLICANT: Nan 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Daignosis and Prognosis
; TITLE OF INVENTION: Diagnosis and Prognosis
; TITLE OF INVENTION: Diagnosis and Prognosis
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR FILING DATE: 2002-06-14
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Best Local Similarity 100.0%; P
Matches 104; Conservative 0;
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US-10-342-887-1901
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Best Local S
Matches 104
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Pred. No. 1.1e-27;
Mismatches 0;
                                                                                                                                                                                                                 Score 104; DB 13;
Pred. No. 1.1e-27;
Mismatches 0;
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US-10-272-411-4

EQUACICA (Application US/10272411

Publication No. US2030100068A1

GENERAL INFORMATION:

APPLICANT: Barnes Jewish Hospital

APPLICANT: Lam, Jonathan

APPLICANT: Lam, Jonathan

APPLICANT: Lam, Jonathan

APPLICANT: Teitelbaum, Steven

TITLE OF INVENTION: RANKL MIMICS AND USES THEREO:

FILE REFERENCE: 60019620-0202

CURRENT APPLICATION NUMBER: US/10/272,411

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 06/329,393

PRIOR FILING DATE: 2001-10-15

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 1643

TYPE: DNA

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: NCBI/ M35592.1

DATABASE ACCESSION NUMBER: NCBI/ M35592.1

DATABASE ENTRY DATE: 2002-05-01

RELEVANT RESIDUES: (1)..(1643)

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: NCBI/ M35592.1

DATABASE BUTRY DATE: 1993-04-27

RELEVANT RESIDUES: (1)..(1643)

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1

DATABASE STRYY DATE: 1993-04-27

RELEVANT RESIDUES: (1)..(1643)

PUBLICATION INFORMATION:

DATABASE BUTRY DATE: 2002-06-01

RELEVANT RESIDUES: (1)..(1643)

PUBLICATION INFORMATION:

DATABASE BUTRY DATE: 1093-04-27

RELEVANT RESIDUES: (1)..(1643)

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1

DATABASE ROTRY DATE: 2002-08-01

RELEVANT RESIDUES: (1)..(1643)
HUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1901
TYPE: DNA
CRGANISM: Homo sapiens
HUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: X01394
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1901
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Best Local Similarity 100.0%;
Matches 104; Conservative 0;
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Best Local Similarity 100.0%;
Matches 104; Conservative 0
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1.1e-27;
nes 0;
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Pred. No. 1.1e-27;
; Mismatches 0;
Sequence 3, Application US/10218547

Publication No. US20030100074A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Endokine Alpha
FILE REFERENCE: PF561
CURRENT APPLICATION NUMBER: US/10/218,547
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-030
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 104; D
Pred. No. 1.1
; Mismatches
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APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND US
FILE REFERENCE: 60019620-0206
CURRENT APPLICATION NUMBER: US/10/272,3
CURRENT FILING DATE: 2003-01-24
PRIOR FILLING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3:1
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1.2e-27;
nes 0;
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Pred. No. 1.1e-27;
Mismatches 0;
                                                                                                                                                                       US20030194721A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09973850
; Publication No. US20020086016A1
; GENERAL INFORMATION:
; APPLICANT: Wunderink, Richard
APPLICANT: Waterer, Grant
; TITLE OF INVENTION: Method for Identifying I
; TITLE OF INVENTION: Pneumonia
; FILE REFERENCE: GCI-0017
; CURRENT APPLICATION NUMBER: US/09/973,850
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/239,133
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying
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US-09-973-850-2
; Sequence 2, Application US/09973850
; Publication No. US20020086016A1
; GENERAL INFORMATION:
; APPLICANT: Wunderink, Richard
; APPLICANT: Waterer, Grant
; TITLE OF INVENTION: Method for Ident:
; TITLE OF INVENTION: Pneumonia
; FILE REFERENCE: GCI-0017
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NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL Program
SEQ ID NO 68
LENGTH: 1666
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte I
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                                                                                                                                                                                                                                                                                                                                     Similarity 100 104; Conservative
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19-973-850-1
                                                                                                                                                                                      ; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1347, 1358
; OTHER INFORMATION: a,
US-10-247-671-68
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US-09-973-850-1
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Matches 104
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Matches 104
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Necrosis Factor-Gamma Beta
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US-10-247-671-68

Sequence 68, Application US/10247671

Publication No. US20030194721A1

GENERAL INFORMATION:

APPLICANT: Mikita, Thomas

APPLICANT: Shiffman, Dov

APPLICANT: Raser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CEL

FILE REFERENCE: PA-0050 US

CURRENT APPLICATION NUMBER: US/10/247,671

CURRENT FILING DATE: 2002-09-18

PRIOR FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               File
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 104; DB 15;
Pred. No. 1.1e-27;
); Mismatches 0;
         RESULT 12
US-10-310-793-9
Sequence 9, Application US/10310793
Publication No. US20030198640A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Chang, Jun
APPLICANT: Nei, Fing
CURRENT APPLICATION NUMBER: G0/336,695
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/314,381
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/216,879
PRIOR APPLICATION NUMBER: 60/216,879
PRIOR APPLICATION NUMBER: 60/216,879
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR APPLICATION NUMBER: 60/132,27
PRIOR APPLICATION NUMBER: 60/132,227
PRIOR PRILING DATE: 2000-02-08
PRIOR FILING DATE: 1999-05-03
PRIOR PRIOR
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Best Local Similarity 100.0%;
Matches 104; Conservative
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; ORGANISM: human
US-10-310-793-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1130
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CURRENT APPLICATION NUMBER: US/09/973,850

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,133

PRIOR PLING DATE: 2000-10-10

NUMBER OF SEQ ID NOS: 3-10-10

LENGTH: 2086

TYPE: DNA

TYPE: DNA

COMMANDE: Parent In version 3.1

SOTUMARE: Parent In version 3.1

LENGTH: 2086

TYPE: DNA

COMMANDE: Parent In version 3.1

COMMANDE: Parent In version 3.1

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version (c) 1993 - 2004
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| Description   | equence 13, Appendence 13, Appendence 1329, Appendence 14, Appendence 11, Appendence 11, Appendence 11, Appendence 11, Appendence 12, Appendence 12, Appendence 13, Appendence 13, Appendence 13, Appendence 12, Appendence 1004, Appendence 10 | equence 30, App |
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| SUMMARIES     |  | -09-479-409-3   |
| DB            | 4          | ო               |
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| Result<br>No. | 000 0 000<br>144444444444444444444444444444  | (1)             |

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Score 104; DB 4; Pred. No. 2.4e-27;

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Query Match Best Local Similarity

; ; ; SEQUENCE DESCRIPTION: SEQ ID NO: 13: US-09-032-297A-13

| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0   |           | RESULT 1<br>US-09-032-<br>; Sequence<br>; Patent h |                    |                   |   |                |               |                    |                                |              |                    |                    |                           |                       | INFO                            |                   |    |                  |         |
|---|-----------|--|--------------------|-------------------|---|----------------|---------------|--------------------|--------------------------------|--------------|--------------------|--------------------|---------------------------|-----------------------|---------------------------------|-------------------|----|------------------|---------|
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| 7   |           | 13<br>Applicat<br>25184<br>ORMATION                | F IN               | OF SEQ            | ADDRESSEE: Bo<br>STREET: 900 1<br>CITY: Ridgef: | PATE: COUNTRY: | ER READ       | OMPUTER<br>PERATIN | PPLICAT                        | LING D       | APPLICA<br>PPLICAT | ILING D            | AME: RO                   | SFERENC<br>MUNICA     | SLEPHON<br>FOR SE               | ENGTH:<br>(PE: nu | 젊  | E TYPE<br>SCRIPT | l       |
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| US - 09 - 4 / | ALIGNMENT | 32297A<br>ake, Steven                              | ton<br>Regulated A | مانانامدودی دو    | ger Ingelheim<br>ıry Road, P.O                  | ates of Ameri  | 1.44 Mb diske | MS DOS             | cessing<br>A:<br>: US/09/032.2 |              | : 60/038,266       | 3-97<br>ION:       | уто <b>пd</b><br>R: 25089 | MBER: 9/121<br>ATION: | -6183<br>3 :<br>S :             |                   | le | •                |         |
| 25 - 10 - 10 - 10 - 10 - 10 - 10 - 10 - 1   | S         | D. Marlin and                                      | poptosis of        | ra ny deme me     | n Corporation<br>). Box 368                     | Ca             | it<br>tte     |                    | 4.66<br>4.66                   | ١            |                    |                    |                           | PCT                   |                                 |                   |    |                  |         |
| Sequence 30, App<br>Sequence 29, App<br>Sequence 29, App<br>Sequence 22, App<br>Sequence 11, App<br>Sequence 17, App<br>Sequence 17, App<br>Sequence 17, App<br>Sequence 17, App<br>Sequence 1, Appl<br>Sequence 1, Appl  |           |  | \$                 | נקשן              |   |                |               |                    |                                |              |                    |                    |                           |                       |                                 |                   |    |                  |         |

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PRINCE APPLICATION NUMBER:
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TYPE: DNA
ORGANISM: Human
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US-09-505-250-4

Sequence 4, Application US/09505250A

Sequence 4, Application US/09505250A

Sequence 4, Application US/09505250A

GENERAL INFORMATION:
APPLICANT: Rosen, Glenn
APPLICANT: Ros, Peter
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
TITLE OF INVENTION: Triptolides and Death Domain Ligands
FILE REFERENCE: SUN-109PRV2

CURRENT APPLICATION NUMBER: US/09/505,250A

CURRENT FILING DATE: 2000-02-15

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 1643
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Pred. No. 3.1e-27;
Mismatches 0
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Pred. No. 3.1e-27;
Mismatches 0
                                                                                                                                                                                                                            (EMBL
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0980
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                              SIRALLE TYPE: UNKNOWN MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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Best Local Similarity 100.0%;
Matches 104; Conservative (
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Best Local Similarity 100.0%;
Matches 104; Conservative (
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (153)...(854)
US-09-505-250-4
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                     CDS
153
                                                                                                                                                                                                                                                                   , NAME/KEY:
, LOCATION:
US-08-880-342-36
                                                                                                                                                                                                                                                      FEATURE:
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Best Local Similarity 100.0%; Pred. No. 3.6e-27
Matches 104; Conservative 0; Mismatches 0
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Pred. No. 3.4e-27;
Mismatches 0
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Sequence 14, Application US/09229151C

Batent No. 6537784

GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Marlin, Steven D.
APPLICANT: Barton, Randall W.
TITLE OF INVENTION: Self-Regulated Apoptosis of FILE REFERENCE: 9/137
CURRENT APPLICATION NUMBER: US/09/229,151C
CURRENT APPLICATION NUMBER: US 60/076,316
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 2.0
SEQ ID NO 14
LENGTH: 2570
US-09-229-151C-13

Sequence 13, Application US/09229151C

Patent No. 6537784

GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Marlin, Steven D.
APPLICANT: Barton, Randall W.
TITLE OF INVENTION: Self-Regulated Apoptosis
FILE REFERENCE: 9/137

CURRENT APPLICATION NUMBER: US/09/229,151C

CURRENT FILING DATE: 1999-01-12
PRIOR FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 2.0

SEQ ID NO 13

LENGTH: 2270
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Best Local Similarity 100
Matches 104; Conservative
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; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: C
US-09-229-151C-14
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; OTHER INFORMATION:
US-09-229-151C-13
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us-09-801-371a-1.rni

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Gaps
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RESULT 8
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF;
; TITLE OF INVENTION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
; LENGTH: 3634
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EDATURE:
NAME/KEY: intron
LOCATION: (1635)..(1821)
FEATURE:
NAME/KEY: exon
LOCATION: (1822)..(1869)
FEATURE:
NAME/KEY: intron
LOCATION: (1870)..(2070)
FEATURE:
NAME/KEY: exon
LOCATION: (2111)..(3381)
FEATURE:
NAME/KEY: exon
LOCATION: (2111)..(3381)
FOURLICATION: NFORMATION:
AUTHORS: Naylor, S.L.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Geeddel, D.V.
AUTHORS: Geeddel, D.V.
AUTHORS: Geeddel, D.V.
AUTHORS: Gray, R.W.
TITLE: Human lymphotoxin and tumor necrosis factor gen
JOURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE BUTRY DATE: 1997-02-17
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(796..981,1589..1634,1822..1869,2171..2592)
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Best Local Similarity 100.0%; Score 104; DB 3
Best Local Similarity 100.0%; Pred. No. 4e-27;
Matches 104; Conservative 0; Mismatches
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(1589)..(1634)
                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (796..981,1589
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(982)..(1588)
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LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY:
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US-09-313-932-1

i Sequence 1, Application US/09313932A

i Sequence 1, Application US/09313932A

i Sequence 1, Application US/09313932A

i GENERAL INFORMATION:

i APPLICANT: Barenda

i APPLICANT: Bennett, C. Frank

i APPLICANT: Bennett, C. Frank

i APPLICANT: Barenda

i APPLICANT: Barenda

i APPLICANT: Bennett, C. Frank

i APPLICANT: Bennett, C. Frank

i TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF.

i TITLE OF INVENTION: EXPRESSION

i TITLE OF INVENTION: EXPRESSION

i FILE REFERENCE: ISPH-0356

i CURRENT FILING DATE: 1999-05-18

i NUMBER OF SEQ ID NOS: 501

i LENGTH: 3634

i LENGTH: 3634
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NAME/KEY: intron
LOCATION: (982). (1588)
FEATURE:
NAME/KEY: exon
LOCATION: (1639)...(1634)
FEATURE:
NAME/KEY: exon
LOCATION: (1635)...(1821)
FEATURE:
NAME/KEY: exon
LOCATION: (1822)...(1869)
FEATURE:
NAME/KEY: intron
LOCATION: (1870)...(2070)
FEATURE:
NAME/KEY: exon
LOCATION: (2171)...(3381)
PUBLICATION: (2171)...(3381)
PUBLICATION: Nedwin, G.E.
AUTHORS: Naylor, S.L.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Pennica, D.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human Lymphotoxin and tumor necrosis:
TITLE: Structure, homology and chromosomal locume: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1
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Best Local Similarity 100.0%; Pred. No. 4e-
Matches 104; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (796..981,1589
FEATURE:
NAME/KEY: exon
LOCATION: (615)..(981)
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1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCC
2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCC

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                                                                AGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTG
                                                                                         AGCCCTGAGGGCCTCTGGGGCTGGAAGGTG
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Pred. No. 13;
0; Mismatches
                                                                                                                                                     US-09-341-587-7/c

US-09-341-587-7/c

Sequence 7, Application US/09341587

Patent No. 6346606

GENERAL INFORMATION:

TITLE OF INVENTION: Protein Containing an SRC

TITLE REFERENCE: 4121-108

CURRENT APPLICATION NUMBER: US/09/341,587

CURRENT FILING DATE: 1999-08-31

EARLIER APPLICATION NUMBER: PCT/DE98/00096

EARLIER FILING DATE: 1998-01-09

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 28720

TYPE: DNA

ORGANISM: Homo sapiens

US-09-341-587-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-818-512-3

US-09-818-512-3

Sequence 3, Application US/09818512

Patent No. 6537780

GENERAL INFORMATION:

APPLICANT: BEASLEY, Ellen et al.

TITLE OF INVENTION: ISOLATED HUMAN ENZYME F

TITLE OF INVENTION: ACID MOLECULES ENCODIN

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001192

CURRENT APPLICATION NUMBER: US/09/818,512

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 116592
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Pred. No.
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Similarity 54.5%;
55; Conservative (
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LOCATION: (1)...(116592)
OTHER INFORMATION: n = A,T,C
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Best Local Similarity 58.3%;
Matches 49; Conservative
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ORGANISM: Human
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Best Local S
Matches 55
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                                                                           RESULT 10
US-09-109-663-34

; Sequence 34, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
; APPLICANT: Tu, Guang-Chou
APPLICANT: Israel, Yedy
; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
; TITLE OF INVENTION: BFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 9855-3U1
; CURRENT APPLICATION NUMBER: US/09/109,663
; CURRENT FILING DATE: 1998-07-03
; EARLIER FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTG
2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTG
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Pred. No. 4e-27;
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US-09-976-594-142/c
; Sequence 142, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A L:
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; RIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SEQ ID NO 142
; LENGTH: 2623
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                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 34
LENGTH: 3634
TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
COTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34
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Similarity 58.9%;
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte I
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; LOCATION: 2612
; OTHER INFORMATION: a, t,
US-09-976-594-142
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US-09-169-768-1
Sequence 1, Application US/09169768
Fatent No. 6492508
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOT A.
APPLICANT: BROKAW, JANE
APPLICANT: BROKAW, JANE
APPLICANT: PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STATE: NY
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                                                                                  RESULT 14
US-09-621-976-19072/c
; Sequence 19072, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 19072
; LENGTH: 412
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ZIP: 11553
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,768
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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Matches '50; Conservative
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; LOCATION: 87,95..98,125,239
; OTHER INFORMATION: n=a, g, US-09-621-976-19072
                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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; TELEPHONE: (516) 228-8484
; TELEFAX: (516) 228-8516
; INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 3170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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Similarity 57.1%;
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ive a | printed, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

N. Geneseq 29Jan04:\*
1: geneseqn1990s:\*
2: geneseqn2000s:\*
4: geneseqn2001as:\*
5: geneseqn2001bs:\*
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| 9          | 76         | 6377    | cf63382 Human TN | cc5789  | ca6494  | cd049   | ad4585  | ad45898 | а£86085 Гутрьо | af57450 | al51863 Human t | a34964 Human a | af21086 Human | bz96780 Human n | 65 Human ad | aa34965 Human | af2108  | af2108 | 67      | 29678   | 475     |
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| 3634       |            | 3634    | 63               | 63      | 3634    | 3634    | 91      | Q<br>H  | 11             | 11      | 11              | 631            | 631           | 631             | 763         | 763           | 63      | 76     | 63      | 763     | 180     |
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# ALIGNMENTS

Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit; RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha; tumour necrosis factor alpha; TNF-alpha; gene therapy; ss. Cis-acting nucleotide sequence derived from human TNF-alpha Ben-Asouli Jarrous N, ВЪ 98IL-00126112 98IL-00126757 99WO-IL000483 & DEV CO. 104 entry) RESULT 1 AAZ99816 ID AAZ99816 standard; RNA; Osman F, WPI; 2000-257000/22. (first (YISS ) YISSUM RES WO200014255-A1. Homo sapiens 07-SEP-1998; 26-OCT-1998; 06-SEP-1999; 12-JUL-2000 16-MAR-2000 Kaempfer R, AAZ99816; 

Cis

Regulation of gene expression by mRNA splicing is carried out using a c-acting nucleotide sequence controlled by phosphorylation of the alphasubunit of eukaryotic initiation factor 2.

75pp; English Claim 4; Page 15;

by a gene removal another gene renders The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gwhich harbours at least one cis-acting nucleotide sequence. This removing the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene render · rng

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.n. The
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     tive to the
splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structur protein) or industrially or agriculturally applicable protein. The present sequence represents a cis-acting nucleotide sequence of the
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Litis;
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host disease, lupus erythematosus, insulin-dependent (type I) diabe mellitus, ankylosing spondylitis, and in particular, rheumatoid arthritis. The use of such chimeric nucleotides offers simpler and cheaper long-term relief, in comparison with existing conventional pharmaceutical and invasive surgery methods
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The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, andiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the constances side effects. The A-containing ONs break down with the constances of decoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA32312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to AAA33992) are specifically claimed ONs from the present invention. N.B.
                                                                                                                                                                                                                                                                                                                                                                                                       Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                  ID NO:2652
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                                                                                   related polynucleotide SEQ
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c rhinitis;
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  match
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ronchitis;
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chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary condition, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAR18434 to AAR21543 represent human polynucleotide the process in the exemplification of the process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; antisense; lung dysfunction; nasal airway dysfunction; antinflammatory; antiallergic; antinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
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                                        Disclosure;
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                         The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, a subject, for reducing or depleting levels of for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, sissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO.
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4.5e-25;
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          12021; 872pp; English
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Best Local Similarity 100.0%; Pred. No. 4.9
Matches 104; Conservative 0; Mismatches
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314. .787
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P-PSDB;
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                                                                                   A human TNF protein which is modified from the sequence shown in AAP80728, including naturally ocurring allelic variants is claimed. Also claimed are: recombinant DNA sequences encoding the protein (AAN80219) and control sequences for expression; a vector; a transformed host cell; a method of producing the protein by culturing the host cell; pharmaceutical compsn. of the protein and a carrier and a method of treating tumour burden with the compsn. The muteins are capable of the range of biological activities exhibited by native TNF but exhibit improved stability and ease of purification
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cloned and expressed in E.coli
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comparable by purification.
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4.7e-25;
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0; Mismatches
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                                                   English.
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   Human tumour necrosis factor muteins activity with improved stability and
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P-PSDB; AAP60655.
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                                          protein,
ink and non-
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penes or derived
AAN60557). Neither of the cysteine residues (69 and 101) in the TNF sequence appears to be involved in disulphide linkages. The patentors claim a novel synthetic mutein of a biologically active hTNF protein, having at least one cysteine residue free from a disulphide link and nessential to the activity and having at least one of the cysteine residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is claimed
                                                                                                                                                                                                                    GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGGCATCTGGGGCCTTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGACATCTGGGGCCTACAACTTGATCCCTGACATCTG
                                                                                                                                                           Length 1585;
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Mismatches 0;
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                                                         GAATICAAACIGGGGCCICCAGAACICACIGGGGCCIACAGCIIIGAICCCIGACAICIG
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                   Length 1585
                                                                                                                                                                                                                                                             Anticancer agent; antitumour; antimalarial; tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U; 0 Other;
 Other;
                                                                                               GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                      Indels
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 0
 Ü,
                  Score 104; DB 7;
Pred. No. 4.7e-25;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   produced by DNA.
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 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.0%; Score 104; DB 1 Similarity 100.0%; Pred. No. 4.7e-2:04; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
H
                                                                                                                                                                                                                                         Sequence encoding tumour necrosis factor (TNF)
Ţ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; 394 G; 361
 371
 Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tavernier JHL,
 C; 389
                                                                                                                                                                                                                                                                                                Location/Qualifiers
158. .859
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalian tumour necrosis factors - hosts transformed with recombinant
                                                                                                                                                                      ВР
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example, Fig 9; 93pp; English.
                                                                                                                                                                      1606
                                                                                                                                                                                                                                                                                                                                                                                                   84US-00684595.
85US-00785847.
86WO-US002133.
                   100.0%;
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 A; 473
                                                                                                                                                                                                                                                                                                                                                                                 85WO-EP000721
                                                                                                                                                                                                           (revised)
(first entry)
                              Similarity 100
4; Conservative
                                                                                                                                                                      CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WC, Fransen LM,
B;
 BP; 352
                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOGEN NV.
FIERS W C.
ALLET B.
BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1986-182891/28
P-PSDB; AAP60531.
                                                                                                                                                                     AAN60446 standard;
  Sequence 1585
                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-1984;
09-OCT-1985;
09-OCT-1986;
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1985;
                                                                                                                                                                                                                                                                                                                                           WO8603751-A
                                                                                                                                                                                                            25-MAR-2003
07-AUG-1991
                    Query Match
Best Local Sim
Matches 104;
                                                                                                                                                                                                                                                                                                                                                             03-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104;
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Best Local S
Matches 104
                                                                                                                                                                                          AAN60446;
                                                                                                  61
                                                                                                                     1063
                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOJ )
(FIER/)
(ALLE/)
(BIOJ )
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Allet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A cDNA clone (AAT15424), p-hTNF-1 (DSM 3160), codes for the human tumour necrosis factor (hTNF) precursor (AAR88590). It was obtd. by screening a human cDNA library with a fragment of mouse TNF cDNA. The isolated cDNA may be linked to expression control sequences from phage T4 or phage lambda (see AAT15402-05 and AAT15425-26) for expression in host cells, esp. Escherichia coli, and commercial-scale prodn. of recombinant TNF of use as an antitumour, anticancer and antimalarial agent. (Updated on 25-MAR-2003 to correct PF field.)
tumour necrosis factor - using recombinant DNA encoding TNF control of T4 or lambda pL-T4 expression control sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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L
                                 phage lambda;
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1;
                                                                                                                                                        CDNA clone p-hTNF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 104; DB
Pred. No. 4.7e-
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G; 361
                                                                                                                                                                        T4;
                                                                                                                                                                        TNF; phage T4 antimalarial;
                                                                                                                                                                                                                Location/Qualifiers
158. .859
/*tag= a
158. .385
/*tag= b
386. .856
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; 394
                                                                                            ВD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       43pp; English
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0
                                                                                            1606
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Similarity 100.0%;
4; Conservative (
                                                                                                                                                        factor
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85US-00785847
                                                                                                                                                                                                                                                                                                                         85US-00811654
                                                                                                                                       entry)
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                                                                                            CDNA;
                                                                                                                                                                      Tumour necrosis factor; antitumour; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                    EH.
                                                                                                                              (revised)
(first en
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                                                                                                                                                         necrosis
                                                                                                                                                                                                                                                                                                                                                                                    Kawashima
                                                                                                                                                                                                                                                                                                                                                                                                    1996-105230/11
B; AAR88590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٠<u>,</u>
                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Fig
                                                                                                                                                                                                                                                                                                                                                                   BIOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1606
                                                                                                                                                         Human tumour
                                                                                                                                                                                                                                                                                                                        20-DEC-1985;
                                                                                                                                                                                                                                                                                                                                        21-DEC-1984;
09-OCT-1985;
                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                      US5487984-A
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Best Local Sim
Matches 104;
                                                                                                                                                                                                                                           sig_peptide
                                                                                                                             25-MAR-2003
23-APR-1996
                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                       0-JAN-1996
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                                                  1135
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                                  61
                                                                                            AAT15424
                                                                                                            AAT15424
 Н
                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
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                107
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A PCR-generated DNA fragment (AAT31021) encoding human tumour necrosis factor (hTNF) (AAW00454). hTNF induces apoptosis and is not known to be induced by hypoxic stress. A -90 bp human metallothionein IIA promoter fragment (see also AAT31003) was inserted upstream of the hTNF gene and the construct was used to transfect mouse C2C12 myoblasts and A431 cells Hypoxia- mediated TNF induction and tumour control were demonstrated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   caused
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injury c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1643;
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                    1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
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                                                                                                                                                                                                                                                                                                                                                                                          linked to HREE -
to reduce tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                element; HREE factor; TNF; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 104; DB 2;
Pred. No. 4.7e-25;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1643 BP; 370 A; 495 C; 398 G; 380
                                                                                                                               clone
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 8; Page 100-101; 118pp; English
                                                                                                                                                enhancer
necrosis
                                                                                                                                                                                                                                                                                                                                                                                        Chimeric gene contg. therapeutic gene expressing SOD etc. in hypoxic tissue ischaemia or reperfusion.
                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                 Location/Qualifiers
153. .854
/*tag= a
                                                                                                                                                                                                                                                                                                                                          Murphy
                                                                                                                               CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٥;
                                                                                                                                                Gene therapy; hypoxia related reperfusion; promoter; tumour
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Best Local Similarity 100.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1643
                                                                                                                               factor
                                                                                                                                                                                                                                                                                95WO-IB000996
                                                                                                                                                                                                                                                                                                   94US-00365486
                                                                      standard; DNA; 1643
                                                                                                                                                                                                                                                                                                                                          Bishopric NH,
                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             animal xenograft model
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.195
ABK13195 standard; DNA;
                                                                                                                               necrosis
                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-321849/32
                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW00454
                                                                                                                                Human tumour
                                                                                                                                                                                                                                                                                                   23-DEC-1994;
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                          WO9620276-A1
                                                                                                                                                                                                                                                                                                                     (STRI ) SRI
                                                                                                                                                                                                                                                                                                                                          Webster KA,
                                                                                                                                                                                                                                                            04-JUL-1996
                                                                                                           26-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypoxia-
                     1135
                                                                      AAT31021
                                                                                                                                                                                                  Key
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ABK1319
ID AB
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GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG

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GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACA

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This invention relates to a novel method for enhanced killing of tumour cells comprising contacting a tumour cell with a synergistic combination of a death domain receptor ligand and a diterpenoid triepoxide. This method has cytostatic activity and works by blocking TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the invention may be used for treating tumours, particularly solid tumours, e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma also neurological malignancies, e.g. non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis chronic lymphocytic leukaemia, palignant cutaneous T-cell lymphoma, lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid lupus erythematosus, lichen planus. The combination may be administered with other active agents, e.g. anti- metastatic, anti-tumour or anti- angiogenic agents. The potent synergy between the diterpenoids and the captube doses, and can sensitise otherwise resistant cells. This sequence represents the human tumour necrosis factor alpha (TNF alpha) DNA. TNF alpha is a ligand for death domain receptors used in the used method of the indication of another propriet is triepoxides to kill tumours the indication with diterpenoid triepoxides to kill tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of tumour combination
                                                                                                                   carcinoma;
                                                                                              TNF; apoptosis; ds; tumour; death domain receptor ligand; diterpencid triepoxide; cytostatic activity; c-IAP2; c-IAP1; carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma; neurological malignancy; haematological malignancy; lichen planus; non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic; malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic; non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour; T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid; discoid lupus erythematosus; human; gene; tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               death domain receptor light of tumor cells.
                                                                     alpha) DNA
                                                                                                                                                                                                                                                                                                                                                          "TNF alpha protein"
                                                                   alpha (TNF
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
153. .854
/*tag= a
/product= "TNF alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of a synergistic combination of diterpenoid triepoxides for killing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANFORD
                                                                     necrosis factor
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99US-0149989P
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-00505250
                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-121125/16
P-PSDB; AAU75065.
                                   (first
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                                                                                                                                                                                                                                                                       sapiens.
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                                                                     Human tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                             5-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                           US6329148-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                   23-APR-2002
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 ABK13195
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                                                                                                                                                                                                                                                                        Ношо
                                                                                                                                                                                                                                                                                                         Key
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New RANKL mimic comprising a core, and at least one external loop, useful for enhancing processes of bone formation or inhibiting bone resorption, thus providing treatments for disease or condition characterized by loss

Teitelbaum SL

ROSS PF,

Lam J,

WPI; 2003-430346/40.

BARNES-JEWISH HOSPITAL

(BARN-)

2002WO-US033022

15-OCT-2002;

24-APR-2003.

WO2003033663-A2

Homo sapiens.

2001US-0329393P

15-OCT-2001;

1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG

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1643

standard; DNA;

ACC57575

RESULT ACC5757

ACC57575;

UXXXX

Polynucleotide encoding tumour necrosis factor superfamily member

(first

28-JUL-2003

Human; RANKL; tumour necrosis factor; osteopathic; bone;

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The present sequence is that of a polynucleotide encoding a non-RANKL member of the tumour necrosis factor (TNF) superfamily. The invention provides non-naturally-occurring proteins that contain one or more of the external surface loops of RANKL (see ABR42066-70) in combination with a heterologous protein core obtained from a non-RANKL member of the TNF superfamily. Also provided are polynucleotides encoding such proteins. The proteins bind to RANK, acting as mimics of RANKL. They can be used tenhance bone formation by either inhibiting bone resorption or inducing osteogenesis, thus providing treatment for diseases or conditions characterised by loss of bone mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; 398 G; 380 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 4.7e-25;
Matches 104; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 48-49; 78pp; English
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Length 1643

Indels

Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Score 104; DB 6;
Best Local Similarity 100.0%; Pred. No. 4.7e-25;
Matches 104; Conservative 0; Mismatches 0;

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GACATCTG

GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCT

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